

H.
Park

1600

RAW SEQUENCE LISTING

DATE: 03/11/2003

PATENT APPLICATION: US/09/677,584

TIME: 10:54:53

Input Set : A:\PTO.VSK.txt

Output Set : N:\CRF4\03112003\I677584.raw

2 <110> APPLICANT: DIVERSA CORPORATION
 3 SHORT, Jay
 W--> 4 <120> TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A SUBSTANTIAL PORTION
 OF A
 W--> 5 STARTING GENOME, COMBINING MUTATIONS, AND OPTIONALLY REPEATING
 7 <130> FILE REFERENCE: DIVER1510WO-1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/677,584
 C--> 10 <141> CURRENT FILING DATE: 2000-09-30
 12 <150> PRIOR APPLICATION NUMBER: US 09/677,584
 13 <151> PRIOR FILING DATE: 2000-09-30
 15 <150> PRIOR APPLICATION NUMBER: US 09/594,459
 16 <151> PRIOR FILING DATE: 2000-06-14
 18 <160> NUMBER OF SEQ ID NOS: 33
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 5818
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Escherichia coli
 27 <400> SEQUENCE: 1

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30	ttccatgtga	cctcctaaca	tggtaacgtt	catgataact	tctgctcttc	atcgtgcggc	120
32	cgactgggct	aaatctgtgt	tctcttcggc	ggcgtgggt	gacctcgcc	gtactgcccg	180
34	cttgggttaac	gtcgcgcgcc	aattggcaaa	atattctggt	aaatcaataa	ccatctcatc	240
36	agagggtagt	gaagccatgc	aggaaggcgc	ttaccgattt	taccgcaatc	ccaacgtttc	300
38	tgccgaggcg	atcagaaagg	ctggcgccat	gcaaacagtc	aagttggctc	aggagtttcc	360
40	cgaactgctg	gccattgagg	acaccacctc	tttgagttat	cgccaccagg	tcgccgaaga	420
42	gcttggaag	ctgggctcta	ttcaggataa	atcccgcgga	tgggtgggttc	actccgttct	480
44	cttgctcgag	gccaccacat	tccgcaccgt	aggattactg	catcaggagt	ggtggatgcg	540
46	cccggatgac	cctgccgatg	cggatgaaaa	ggagagtggc	aaatggctgg	cagcggccgc	600
48	aactagccgg	ttacgcgatg	gcagcatgat	gagcaacgtg	attgcggtct	gtgaccgcga	660
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54	ccaaccggag	ttgggtggct	atcagatcag	cattccgcaa	aagggcgtgg	tggataaacg	840
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68	cacgctggcg	caagcactca	ggcgcgcaag	gctgctaaag	gaagcggaac	acgtagaaag	1260
70	ccagtccgca	gaaacggtgc	tgaccccgga	tgaatgtcag	ctactgggct	atctggacaa	1320
72	gggaaaacgc	aagcgcaaag	agaaagcagg	tagcttgtag	tgggcttaca	tggcgatagc	1380
74	tagactgggc	ggttttatgg	acagcaagcg	aaccggaatt	gccagctggg	gcgccctctg	1440
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P.6

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82 gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca gcgcaggggc 1680
84 gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg caggacgagg 1740
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92 atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc atcgagcgag 1980
94 cacgtactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa gagcatcagg 2040
96 ggctcgcgcc agccgaactg ttccgcaggc tcaaggcgcg catgcccgac ggcgaggatc 2100
98 tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat ggccgctttt 2160
100 ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac atagcgttgg 2220
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168 gaacagcgcg ttggggagca gctcgccagg acggtgcgcg gtggcgcggt gtcttgggag 4260
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172 cagatccttg gcggcaagaa agccatccag ttacttttgc agggcttccc aaccttccca 4380
174 gagggcgccc cagctggcaa ttccggttcg cttgctgtcc ataaaaccgc ccagctctagc 4440

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176 tatcgccatg taagcccact gcaagctacc tgctttctct ttgcgcttgc gttttccctt 4500
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180 ttctacgtgt tccgcttctt ttagcagccc ttgcgcccctg agtgcttgcg gcagcgtgaa 4620
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216 ggcagtacgg cgaggatcac ccagcgccgc cgaagagAAC acagatttag cccagtcggc 5700
218 cgcacgatga agagcagaag ttatcatgaa cgttaccatg ttaggagggtc acatggaagt 5760
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223 <210> SEQ ID NO: 2

224 <211> LENGTH: 476

225 <212> TYPE: PRT

226 <213> ORGANISM: Escherichia coli

228 <400> SEQUENCE: 2

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230 Met Ile Thr Ser Ala Leu His Arg Ala Ala Asp Trp Ala Lys Ser Val
231 1 5 10 15
233 Phe Ser Ser Ala Ala Leu Gly Asp Pro Arg Arg Thr Ala Arg Leu Val
234 20 25 30
236 Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile
237 35 40 45
239 Ser Ser Glu Gly Ser Glu Ala Met Gln Glu Gly Ala Tyr Arg Phe Tyr
240 50 55 60
242 Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met
243 65 70 75 80
245 Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu
246 85 90 95
248 Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly
249 100 105 110
251 Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser
252 115 120 125
254 Val Leu Leu Leu Glu Ala Thr Phe Arg Thr Val Gly Leu Leu His
255 130 135 140
257 Gln Glu Trp Trp Met Arg Pro Asp Asp Pro Ala Asp Ala Asp Glu Lys
258 145 150 155 160
260 Glu Ser Gly Lys Trp Leu Ala Ala Ala Thr Ser Arg Leu Arg Met

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261          165          170          175
263 Gly Ser Met Met Ser Asn Val Ile Ala Val Cys Asp Arg Glu Ala Asp
264          180          185          190
266 Ile His Ala Tyr Leu Gln Asp Arg Leu Ala His Asn Glu Arg Phe Val
267          195          200          205
269 Val Arg Ser Lys His Pro Arg Lys Asp Val Glu Ser Gly Leu Tyr Leu
270          210          215          220
272 Ile Asp His Leu Lys Asn Gln Pro Glu Leu Gly Gly Tyr Gln Ile Ser
273 225          230          235          240
275 Ile Pro Gln Lys Gly Val Val Asp Lys Arg Gly Lys Arg Lys Asn Arg
276          245          250          255
278 Pro Ala Arg Lys Ala Ser Leu Ser Leu Arg Ser Gly Arg Ile Thr Leu
279          260          265          270
281 Lys Gln Gly Asn Ile Thr Leu Asn Ala Val Leu Ala Glu Glu Ile Asn
282          275          280          285
284 Pro Pro Lys Gly Glu Thr Pro Leu Lys Trp Leu Leu Leu Thr Gly Glu
285          290          295          300
287 Pro Val Glu Ser Leu Ala Gln Ala Leu Arg Val Ile Asp Ile Tyr Thr
288 305          310          315          320
290 His Arg Trp Arg Ile Glu Glu Phe His Lys Ala Trp Lys Thr Gly Ala
291          325          330          335
293 Gly Ala Glu Arg Gln Arg Met Glu Glu Pro Asp Asn Leu Glu Arg Met
294          340          345          350
296 Val Ser Ile Leu Ser Phe Val Ala Val Arg Leu Leu Gln Leu Arg Glu
297          355          360          365
299 Ser Phe Thr Leu Pro Gln Ala Leu Arg Ala Gln Gly Leu Leu Lys Glu
300          370          375          380
302 Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp
303 385          390          395          400
305 Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys
306          405          410          415
308 Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu
309          420          425          430
311 Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala
312          435          440          445
314 Leu Trp Glu Gly Trp Glu Ala Leu Gln Ser Lys Leu Asp Gly Phe Leu
315          450          455          460
317 Ala Ala Lys Asp Leu Met Ala Gln Gly Ile Lys Ile
318 465          470          475

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320 <210> SEQ ID NO: 3

321 <211> LENGTH: 30

322 <212> TYPE: DNA

323 <213> ORGANISM: Artificial sequence

325 <220> FEATURE:

326 <223> OTHER INFORMATION: Defined sequence kernel

328 <220> FEATURE:

329 <221> NAME/KEY: misc_feature

330 <222> LOCATION: (1)..(30)

331 <223> OTHER INFORMATION: n is A, T, G, or C

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333 <400> SEQUENCE: 3
W--> 334 nnknknknkn nkknknknkn knknknknkn 30
337 <210> SEQ ID NO: 4
338 <211> LENGTH: 30
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Defined sequence kernel
345 <220> FEATURE:
346 <221> NAME/KEY: misc_feature
347 <222> LOCATION: (1)..(30)
348 <223> OTHER INFORMATION: n is A, T, G, or C
350 <400> SEQUENCE: 4
W--> 351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 30
354 <210> SEQ ID NO: 5
355 <211> LENGTH: 5
356 <212> TYPE: PRT
357 <213> ORGANISM: Artificial sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: Antibody spacer peptide. The entire peptide sequence can be
361     repeated more than one time
363 <400> SEQUENCE: 5
365 Gly Gly Gly Gly Ser
366 1      5
368 <210> SEQ ID NO: 6
369 <211> LENGTH: 14
370 <212> TYPE: DNA
371 <213> ORGANISM: Artificial sequence
373 <220> FEATURE:
374 <223> OTHER INFORMATION: Tetradecanucleotide d
376 <400> SEQUENCE: 6
377 catgccatgg catg 14
380 <210> SEQ ID NO: 7
381 <211> LENGTH: 21
382 <212> TYPE: DNA
383 <213> ORGANISM: Artificial sequence
385 <220> FEATURE:
386 <223> OTHER INFORMATION: 21-mer d
388 <400> SEQUENCE: 7
389 aaattgtgca catcctgcag c 21
392 <210> SEQ ID NO: 8
393 <211> LENGTH: 12
394 <212> TYPE: DNA
395 <213> ORGANISM: Artificial sequence
397 <220> FEATURE:
398 <223> OTHER INFORMATION: 12-mer target DNA
400 <400> SEQUENCE: 8
401 agcctagctg aa 12
404 <210> SEQ ID NO: 9

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,2,4,5,7,8,10,11,13,14,16,17,19,20,22,23,25,26,28,29
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Seq#:10; Xaa Pos. 3
Seq#:12; Xaa Pos. 2
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Seq#:17; N Pos. 82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100
Seq#:17; N Pos. 101,102,103,104,105,106,107,108,109,110,111,112,113,114,115
Seq#:17; N Pos. 116,117,118,119,120,121

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\03112003\I677584.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17